Amendments to the Claims

This Listing of Claims will replace all prior versions, and listings, of claims in the application.

Listing of Claims

1. (Previously Presented) A method for generating a molecular profile of genomic DNA by hybridization of a genomic DNA target to a plurality of immobilized nucleic acid probes, wherein the plurality is a collection of clones that represent all of a chromosome or a genome of an organism, the method comprising:

(a) providing the plurality of nucleic acid probes comprising a plurality of immobilized nucleic acid segments in an array with each probe at a known location, wherein each probe is a member of a genomic library cloned in a vector and each probe is the vector having a cloned nucleic acid insert greater than 50 kilobases, wherein the plurality of probes represents all of the chromosome or the genome;

(b) contacting the immobilized probes with a sample of target nucleic acid comprising fragments of genomic nucleic acid,

wherein said fragments include both strands of a double-stranded genomic DNA fragment and include at least 30% repetitive sequences, and

wherein both strands are labeled with a detectable moiety, wherein each labeled fragment consists of a length smaller than 200 bases, and the contacting is under conditions allowing specific hybridization of both strands of the labeled fragment of the target nucleic acid to the probe nucleic acid; and

(c) observing an amount and location of labeled genomic nucleic acid hybridized to each immobilized probe, to detect regions of amplification or deletion in the sample, wherein positional information of clones on the arrays and chromosomes is correlated,

wherein said method results in less aggregating hybridization to said probes relative to hybridization of said target genomic nucleic acid to said probes using target nucleic acids with labeled fragments of length greater than 200 bases,

or said method results in less background relative to hybridization of said target genomic nucleic acid using target nucleic acids with labeled fragments of length greater than 200 bases,

thereby generating a molecular profile of the chromosome or genome of the sample genomic nucleic acid.

2. (Previously presented) The method of claim 1, wherein each labeled fragment consists of a length no more than 150 bases.

3. (Previously presented) The method of claim 2, wherein each labeled fragment consists of a length no more than 100 bases.

4. (Previously presented) The method of claim 3, wherein each labeled fragment consists of a length no more than 50 bases.

5. (Previously presented) The method of claim 4, wherein each labeled fragment consists of a length no more than 30 bases.

6. (Previously presented) The method of claim 2, wherein each labeled fragment consists of a length between 30 bases and 150 bases.

7. (Previously presented) The method of claim 1, wherein the sample of target genomic nucleic acid is prepared using a procedure selected from the group consisting of random priming, nick translation, and amplification, of a sample of genomic nucleic acid to generate segments of target genomic nucleic acid; followed by a step comprising fragmentation or enzymatic digestion, or both, of the segments to generate a sample of target genomic nucleic acid consisting of sizes smaller than 200 bases.

8. (Previously presented) The method of claim 7, wherein the random priming, nick translation, or amplification, of the sample of genomic nucleic acid to generate segments

of target genomic nucleic acid incorporates detectably labeled base pairs into the segments.

9. (Previously presented) The method of claim 8, wherein the detectable label comprises Cy3™ or Cy5™.

10. (Previously presented) The method of claim 1, further comprising prior to step (b), fragmenting the sample of target genomic nucleic acid to sizes smaller than about 200 bases by DNase enzyme digestion.

11. (Previously presented) The method of claim 1, further comprising prior to step (b), fragmenting the sample of target genomic nucleic acid to sizes smaller than about 200 bases by applying shearing forces sufficient to fragment genomic DNA followed by DNase enzyme digestion of the sheared DNA.

12. (Original) The method of claim 1, wherein the conditions allowing hybridization of the target nucleic acid to the probe nucleic acid comprise stringent hybridization conditions.

13. (Original) The method of claim 12, wherein the stringent hybridization conditions comprise a temperature of about 60°C to about 65°C.

14. (Original) The method of claim 1, wherein the target nucleic acid consists essentially of DNA derived from a human.

Claims 15-16 (cancelled)

17. (Previously presented) The method of claim 1, wherein the chromosome or genome is derived from a human.

Claims 18-66 (cancelled)

67. (Previously presented) The method of claim 72, wherein the sample of target genomic nucleic acid consists essentially of one chromosome.

68. (Previously presented) The method of claim 72, wherein the sample of target genomic nucleic acid comprises a complete genome.

69. (cancelled)

70. (cancelled)

71. (cancelled)

72. (Previously presented) The method of claim 1, wherein said fragments of genomic nucleic acid comprise nucleic acids from all of one or more chromosomes of said organism.

73. (New) A method of detecting sequences in a nucleic acid sample, the method comprising the steps of exposing a labeled nucleic acid sample to an array of immobilized nucleic acids, under dynamic humidity conditions, and determining a molecular profile.

74. (New) The method of claim 73, wherein the step of determining the molecular profile comprises comparing a test sample of labeled nucleic acids that are bound to the array of immobilized nucleic acids with a control sample of nucleic acids that are bound to the array of immobilized nucleic acids.

75. (New) The method of claim 73, wherein the labeled nucleic acid sample comprises nucleic acid fragments of less than about 200 bases.

76. (New) A method of detecting sequences in a nucleic acid sample comprising the steps of:

labeling a nucleic acid test sample with a first detectable moiety to provide a labeled nucleic acid test sample, wherein the nucleic acid test sample comprises nucleic acid fragments of less than about 200 bases;

labeling a nucleic acid control sample with a second detectable moiety to provide a labeled nucleic acid control sample, wherein the nucleic acid control sample comprises nucleic acid fragments of less than about 200 bases;

exposing the labeled nucleic acid test sample and the labeled nucleic acid control sample to an array of immobilized nucleic acids in a dynamic humidity environment; and

detecting, on the array of immobilized nucleic acids, the labeled nucleic acid test sample and the labeled nucleic acid control sample.

77. (New) The method of claim 76, further comprising the step of configuring the array of immobilized nucleic acids with at least two bacterial artificial chromosomes.

78. (New) The method of claim 76, further comprising the step of treating a nucleic acid test sample to form nucleic acid fragments of less than about 200 bases.

79. (New) The method of claim 76, further comprising the step of treating a nucleic acid control sample to form nucleic acid fragments of less than about 200 bases.

80. (New) The method of claim 76, wherein the step of exposing further comprises exposing the labeled nucleic acid test sample and the labeled nucleic acid control sample to an array of immobilized nucleic acids that is in molar excess as compared to the labeled nucleic acid control sample and the labeled nucleic acid test sample.

81. (New) The method of claim 76, wherein the step of exposing further comprises exposing the labeled nucleic acid test sample and the labeled nucleic acid control sample to the array of immobilized nucleic acids in a dynamic temperature environment.

82. (New) The method of claim 76, further comprising the step of washing the array of immobilized nucleic acids with a solution comprising an antioxidant.

83. (New) The method of claim 76, further comprising the steps of introducing the array of immobilized nucleic acids into a humidity-controlled housing, controlling a humidity within the humidity-controlled housing, and exposing the labeled nucleic acid test sample and the labeled nucleic acid control sample to the array of immobilized nucleic acids in the presence of controlled humidity in the humidity-controlled housing.

84. (New) The method of claim 78, wherein the nucleic acid test sample comprises human-derived DNA.

85. (New) The method of claim 76, wherein the first detectable moiety comprises a first fluorescent dye and the second detectable moiety comprises a second fluorescent dye.

86. (New) A kit for detecting sequences in a nucleic acid sample comprising:

a slide having an array of immobilized nucleic acids, wherein the array comprises at least two bacterial artificial chromosomes;

a hybridization buffer;

a labeling buffer; and

instructions for using the slide to generate a molecular profile, comprising instructions for using the slide and the hybridization buffer to provide a humidity gradient in a humidity-controlled environment.

87. (New) The kit of claim 86, wherein the hybridization buffer comprises an antioxidant.

88. (New) The kit of claim 86, further comprising a housing for controlling humidity.

89. (New) The kit of claim 86, further comprising a housing for controlling temperature.

90. (New) The kit of claim 86, further comprising a control nucleic acid sample comprising detectably labeled nucleic acid fragments, wherein each fragment is less than about 200 bases.

91. (New) The kit of claim 90, wherein the detectably labeled nucleic acid fragments comprise a fluorescent dye.

92. (New) The kit of claim 91, wherein the control nucleic acid sample further comprises an antioxidant.

93. (New) The kit of claim 86, further comprising a wash solution.

94. (New) The kit of claim 93, wherein the wash solution comprises an antioxidant.